otherwise, please charge the required fee to Pennie & Edmonds LLP Deposit Account No. 16-1150.

IN THIS FILE:

Please correct the correspondence address to be as indicated in the Declaration and Power of Attorney submitted December 15, 2000:

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IN THE SPECIFICATION:

Please amend the specification as follows:

On page 9, line 9, please replace the paragraph beginning "**Figure 2A-2C.** " with the following paragraph:

-- **Figure 2A-2C.** Molecular Cloning of the *SHR* Gene. (A) The candidate band of En hybridization cosegregating with the *shr* mutant phenotype is indicated (arrow). A similar size band is found in one of the homozygous wild-type plants (line 52). PCR analysis of the En-*SHR* junction in this line indicated that the similar molecular weight band does not correspond to the band observed in the homozygous mutants. Numbers above the gel lanes indicate individual plants of the segregating population. Molecular size markers are indicated on the left. (B) Alignment of the deduced amino acid sequence of the "VHIID domains" of five functionally characterized GRAS family genes *(Ls:* Schumacher et al., 1999, Proc. Natl. Acad. Sci. USA 96, 290-295 (SEQ ID NO: 5); *GAI:* Peng et al., 1997, Nature *400,* 256-261 (SEQ ID NO: 6); *RGA:* Silverstone et al., 1998, Plant Cell *10,* 155-169 (SEQ ID NO: 7); *SCR:* Di Laurenzio et al., 1996 Cell *86,* 423-433 (SEQ ID NO: 8)). Numbers before the sequence indicate the position of the first amino acid of the alignment in the corresponding position in the proteins. Conserved amino acids are shown in bold. *SHR* (SEQ ID NO: 9) is not highly similar to any other functionally characterized GRAS gene. (C) Mutation sites in *shr* alleles. Note that *shr-4* has a duplication of nucleotide triplets (TAG; underlined) at the En insertion site, while the En insertion in *shr-3* did not result in an alteration of the host sequence. *shr-1*, which has a 50 nucleotide base pair deletion, has a

deletion from the threonine at position 408 and includes the cysteine at position 424 of the native SHR sequence. Thus, the remaining sequence is GATGAGTTC....ATGGGAAGAGA.

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On page 10, line 13, please replace the paragraph beginning "**Figure 5A-5C.** " with the following paragraph:

-- **Figure 5A-5C.** *SCR* Expression in *shr* Background. (A) *SCR* RNA accumulation in seedling roots. Northern blot analysis was performed with total RNA from 12-day-old wild-type, *shr-1,* and *shr-2* root tissues hybridized with a *SCR* gene-specific probe. The same blot was hybridized with a *GDH1*(Melo-Oliveira et al., 1996, Proc. Natl. Acad. Sci. USA *93,* 4718-4723) gene-specific probe as a loading control. (B and C) Expression of *SCR::GFP* in the primary root. GFP expression in (B) wild-type and(C) *shr-2* seedling roots harboring the *SCR::GFP* transgene indicating that the *shr* mutation results in reduced expression from the *SCR* promoter. Abbreviations as above.--

On page 27, line 31, through page 28, line 7, please replace the paragraph beginning "In a specific embodiment of the invention, a polypeptide containing" with the following paragraph:

-- In a specific embodiment of the invention, a polypeptide containing at least 10 (continuous) amino acids of the SHR protein is provided. In other embodiments, the polypeptide may contain at least 20 or 50 amino acids. In specific embodiments, such polypeptides do not contain more than 100, 150 or 200 amino acids. Derivatives or analogs of the polypeptides include, but are not limited to, molecules containing regions that are substantially homologous to the SHR protein or fragments thereof (*e.g.*, in various embodiments, at least 60% or 70% or 80% or 90% or 95% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art) or product encoded by a polynucleotide that is capable of hybridizing to a naturally-occurring coding sequence, under highly stringent, moderately stringent, or low stringent conditions. Percent homology may be determined, for example, by comparing sequence information using the BLAST or GAP programs described *supra*.--

On page 38, line 32, through page 39, line 18, please replace the paragraph beginning "Additionally, recombinant antibodies" with the following paragraph:

-- Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, *e.g.*, Cabilly *et al.*, U.S. Patent No. 4,816,567; and Boss *et al.*, U.S. Patent No. 4,816397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarity determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, *e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu *et al.* (1987) *J. Immunol.* 139:3521-3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.* (1987) *Canc. Res.* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; and Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80:1553-1559); Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J. Immunol.* 141:4053-4060.--

On page 62, line 9, please replace the paragraph beginning "The segregating population" with the following paragraph:

-- The segregating population representing the progeny of a *shr-3* heterozygote was genotyped based on phenotype and a DNA sample was extracted from the same individuals for Southern analysis. An end fragment (generated with oligos: En7631 5'-GGCTCACATCATGCTAGTCC- 3' (SEQ ID NO: 10) and En8183 5'-GTTGACCGACACTCTTAGCC -3' (SEQ ID NO: 11)) of the En transposon was used as

probe. A band present in all mutants was identified in lanes corresponding to EcoRV digested DNA (Fig. 3a). A band with identical segregation pattern in the population was observed with EcoRI digestion. In this case the fragment size was 2.6 kb, indicating that the plant derived part of the sequence was about 200 bp.--

On page 62, line 17, please replace the paragraph beginning "The 2.6 kb EcoRI fragment" with the following paragraph:

-- The 2.6 kb EcoRI fragment was isolated from an agarose gel. Inverse PCR was performed (essentially as described by Long et al., 1993, Proc. Natl. Acad. Sci. USA *90,* 10370-10374) using En sequences as a basis with primers 5'-TCTATACGAATAAGAGCGTCC- 3' (fwd) (SEQ ID NO: 12) and 5'-TATTCGCGTCACAATAGTTCC-3' (rev) (SEQ ID NO: 13). An amplification product of approximately 500 bp was obtained, subcloned into a pCRII vector and sequenced.--

On page 63, line 10, please replace the paragraph beginning "The 35S::SHR construct" with the following paragraph:

-- The 35S::SHR construct was made by placing the protein-coding region of *SHR* between the CaMV 35S promoter and the nopaline synthase polyadenylation sequence. The SHR-coding region as well as 31 bp from the 3'UTR were first amplified by PCR with the primers 5'- CAGTCGACTAGTCATATGGATACTCTCTTTAGATTA-3' (SEQ ID NO: 14) and 5'-TGTGGAATTGTGAGCCG-3' (SEQ ID NO: 15) using the 2.8-kb subclone of the *SHR* genomic region as a template. The former primer removed an Spe I site at codon 7 of *SHR,* while creating new Spe I and Nde I sites around the first ATG. These mutations did not alter the encoded amino acid sequence. The latter primer was designed to anneal to downstream vector sequence in the template subclone. The PCR amplified DNA fragment was cloned into pCR2.1 (Invitrogen) and sequenced. The SHR-coding region was excised as an Spe I fragment and inserted into the Xba I site of plasmid W104. The resulting plasmid was transformed into *Agrobacterium tumefaciens* (LBA4404) and used to transform wild-type *Arabidopsis* plants (Col) by the floral dipping method (Clough and Bent, 1998, Plant J. *16,* 735-743).--

On page 63, line 26, through page 64, line 3, please replace the paragraph beginning "Histochemical analysis using" with the following paragraph:

-- Histochemical analysis using monoclonal antibodies (JIM13 and CCRC-M2 antibodies) was performed essentially as described (Di Laurenzio et al., 1996, Cell *86,* 423-433). For the construction of the *SHR* promoter:: β-glucuronidase (GUS) marker gene line, the 2.5 kb region upstream of the *SHR* translational start site was amplified by PCR using the primers: 5'-CGGGATCCAGAAGCAGAGCGTGGGGTTTC-3 '(fwd) (SEQ ID NO: 16) and 5'-CGGGATCCTTTTAATGAATAAGAAAATG-3' (rev) (SEQ ID NO: 17) (GGATCC BamHI site). The 2.5 kb PCR fragment was inserted into the pCR 2.1 vector using the TA cloning kit (Invitrogen) and, after BamHI digestion, it was subcloned into the BamHI site upstream of the GUS coding region in pBI101 (Clontech). This binary vector was used to generate transgenic plants as described above. T1 seeds were collected in separate pools and transgenic plants were selected by planting on media containing kanamycin (50 μg/ml). GUS staining of the *SHR::GUS* line was performed as described previously (Malamy and Benfey, 1997, Development *124,* 33-44). In situ hybridization analysis was performed essentially as described in Di Laurenzio et al. (1996), Cell *86,* 423-433.--

IN THE CLAIMS

Please amend claims 2 and 6 to read as follows:

2 (Amended). The isolated nucleic acid molecule of claim 1, wherein said short-root protein comprises the amino acid sequence of SEQ ID NO:2.

6 (Amended). A recombinant vector comprising the nucleic acid molecule of claim 5.

REMARKS

Applicants respectfully draw the Examiner's attention to the first (cover) page of the Office Action mailed June 6, 2001, in which the party to whom correspondence concerning documents should be mailed is indicated erroneously as:

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